

REMARKS

Applicants submit the following amendments to fulfill the requirements of 37 C.F.R. §1.821-1.825. These amendments replace the original Sequence Listing with an amended substitute Sequence Listing, and amend references to sequence identifiers in the specification and in Figure 11.

Figure 8 depicts a discontinuous nucleic acid sequence with a 5' and 3' region. As currently amended, the 5' region is labeled as SEQ ID NO:18 and the 3' region is labeled as SEQ ID NO:167. The amino acid sequence encoded by SEQ ID NO:18 is labeled as SEQ ID NO:19. The amino acid sequence encoded by SEQ ID NO:167 is labeled as SEQ ID NO:168.

Figure 11 has been amended to refer to SEQ ID NOs:169-180 to distinguish them from the sequences at pages 47-50 of the specification. A substitute Figure 11 containing amended sequence identifiers is filed herewith.

Applicant : Jin-Soo Kim et al.
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Attached hereto is a marked-up version of the changes made to the specification and drawings by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket number 12279-002001.

Respectfully submitted,

Date:

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Janis K. Fraser, Ph.D., J.D.
Reg. No. 34,819

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

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Version With Marked Changes

In the specification:

Paragraph beginning at page 13, line 1, has been amended as follows:

Fig 8. is a diagram of pPCFMS-Zif, a plasmid that can be used for the construction of a library of hybrid plasmids [(SEQ ID NOs:18 and 19)]. The region 5' of the Zif 268 insertion site corresponds to SEQ ID NO:18, and the amino acid sequence shown below this region corresponds to SEQ ID NO:19. The region 3' of the Zif268 insertion site corresponds to SEQ ID NO:167, and the amino acid sequence shown below this region corresponds to SEQ ID NO:168.

Paragraph beginning at page 13, line 10, has been amended as follows:

Fig. 11 is a list of some DNA sequences of zinc finger domains selected by the *in vivo* system from a zinc finger library derived from the human genome and amino acid sequences encoded by the DNA sequences (SEQ ID NOs:[22-33] 169-180). The DNA sequences corresponding to the degenerate PCR primers used to amplify DNA segments encoding zinc finger domains from the human genome are underlined. The four potential base-contacting positions are indicated, and the amino acid residues are shown in bold. The two Cys residues and two His residues that are expected to coordinate with the zinc ion are shown in italics.



Figure 11

Version With Marked Changes

CSNR:

T G Q K P Y K C K Q C G K A F G C P S
ACC GGG CAG AAA CCG TAC AAA TGT AAG CAA TGT GGG AAA GCT TTT GGA TGT CCC TCA
-1 2
N L R R H G R T H T G E K P R (SEQ ID NO:23 170)
AAC CTT CGA AGG CAT GGA AGG ACT CAC ACC GGC GAG AAA CCG CGG (SEQ ID NO:22 169)
3 6

HSNK:

T G E K P Y K C K E C G K A F N H S S
ACC GGG GAG AAG CCA TAC AAG TGT AAG GAG TGT GGG AAA GCC TTC AAC CAC AGC TCC
-1 2
N F N K H H R I H T G E K P R (SEQ ID NO:25 172)
AAC TTC AAT AAA CAC CAC AGA ATC CAC ACC GGC GAA AAG CCG CGG (SEQ ID NO:24 171)
3 6

SSNR:

T G E R P F E C K E C G K A F S S G S
ACC GGG GAG AGG CCA TTT GAA TGT AAG GAA TGT GGG AAA GCC TTT AGT AGT GGT TCA
-1 2
N F T R H Q R I H T G E K P R (SEQ ID NO:27 174)
AAC TTC ACT CGA CAT CAG AGA ATT CAC ACC GGT GAA AAG CCG CGG (SEQ ID NO:26 173)
3 6

RDER:

T G Q K P Y V C D V E G C T W K F A R
ACC GGG CAG AAG CCA TAC GTA TGC GAT GTA GAG GGA TGT ACG TGG AAA TTT GCC CGC
-1
S D E L N R H K K R H T G E R P R (SEQ ID NO:29 176)
TCA GAT GAG CTC AAC AGA CAC AAG AAA AGG CAC ACC GGC GAA AGA CCG CGG (SEQ ID NO:28 175)
2 3 6

QSTV:

T G E R P Y E C N E C G K A F A Q N S
ACC GGG GAG AGA CCT TAC GAG TGT AAT GAA TGC GGG AAA GCT TTT GCC CAA AAT TCA
-1 2
T L R V H Q R I H T G E K P R (SEQ ID NO:34 178)
ACT CTC AGA GTA CAC CAG AGA ATT CAC ACC GGC GAA AAG CCG CGG (SEQ ID NO:30 177)
3 6

VSTR:

T G E R P Y E C N Y C G K T F S V S S
ACC GGG GAG AGG CCT TAT GAG TGT AAT TAC TGT GGA AAA ACC TTT AGT GTG AGC TCA
-1 2
T L I R H Q R I H T G E R P R (SEQ ID NO:33 180)
ACC CTT ATT AGA CAT CAG AGA ATC CAC ACC GGC GAG AGA CCG CGG (SEQ ID NO:32 179)
3 6